compomer witnesses; and...determining a reduced set of sequence variation candidates corresponding to the compomer witnesses.

(2) The limitations expressed in claims 38 and 39 regarding the percentage of the mixture of target nucleic acids that contain the sequence variation.

With regard to the first limitation (regarding compomers, etc.), while Zabeau does not incorporate this step into the preferred embodiments of his method, he does teach that mass spectroscopy-based assays are used to "confirm the base composition of small fragments whose masses are determined with sufficient accuracy to reduce the number of possible compositional isomers" (page 4, lines 18-20). This fits precisely Applicant's definition of "compomer", "compomer witness" and "reduced set of sequence variation candidates" found in paragraphs [0107], [0108] and [[0123], respectively, of the specification.

Therefore, it would have been *prima facie* obvious to one of ordinary skill in the art at the time the invention of the instant application was made to modify the method of Zabeau to incorporate the optional step taught by Zabeau of determining the base composition to reduce the number of possible compositional isomers (i.e. compomers). One of skill in the art would have been motivated to do this in cases where known polymorphisms were being assessed, because this would require fewer cleavage reactions than would be required for the actual *unequivocal* determination of the sequence of the target. This modification would in turn simplify the assay as well as reduce the time and expense of the assay.